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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/989,025A

DATE: 07/10/2002
 TIME: 10:47:24

Input Set : A:\PTO.PG.txt
 Output Set: N:\CRF3\07102002\I989025A.raw

3 <110> APPLICANT: NAKAI, JUNICHI
 5 <120> TITLE OF INVENTION: METHOD FOR PRODUCING A BIOSENSOR PROTEIN CAPABLE OF
 REGULATING A
 6 FLUORESCENCE PROPERTY OF GREEN FLUORESCENT PROTEIN, AND THE BIOSENSOR PROTEIN
 7 PRODUCED BY THE METHOD
 9 <130> FILE REFERENCE: 216339US0
 11 <140> CURRENT APPLICATION NUMBER: 09/989,025A
 12 <141> CURRENT FILING DATE: 2001-11-21
 14 <150> PRIOR APPLICATION NUMBER: JP/2000-356047
 15 <151> PRIOR FILING DATE: 2000-11-22
 17 <160> NUMBER OF SEQ ID NOS: 17
 19 <170> SOFTWARE: PatentIn version 3.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 717
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Aequorea victoria
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (1)..(717)
 29 <223> OTHER INFORMATION:
 32 <400> SEQUENCE: 1
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 35 1 5 10 15
 37 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 38 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 39 20 25 30
 41 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
 42 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 43 35 40 45
 45 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
 46 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 47 50 55 60
 49 acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag cag 240
 50 Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 51 65 70 75 80
 53 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 54 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 55 85 90 95
 57 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 58 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 59 100 105 110
 61 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 62 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile

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63	115	120	125	
65	gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac			432
66	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn			
67	130	135	140	
69	tac aac agc cac aac gtc tat atc atg gcc gac aag cag aac ggc			480
70	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly			
71	145	150	155	160
73	atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg			528
74	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val			
75	165	170	175	
77	cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc			576
78	Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro			
79	180	185	190	
81	gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc			624
82	Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser			
83	195	200	205	
85	aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg			672
86	Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val			
87	210	215	220	
89	acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag taa			717
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94	<210> SEQ ID NO: 2			
95	<211> LENGTH: 238			
96	<212> TYPE: PRT			
97	<213> ORGANISM: Aequorea victoria			
99	<400> SEQUENCE: 2			
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102	1	5	10	15
105	Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu			
106	20	25	30	
109	Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys			
110	35	40	45	
113	Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu			
114	50	55	60	
117	Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln			
118	65	70	75	80
121	His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg			
122	85	90	95	
125	Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val			
126	100	105	110	
129	Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile			
130	115	120	125	
133	Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn			
134	130	135	140	
137	Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly			
138	145	150	155	160
141	Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val			
142	165	170	175	

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145 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 146 180 185 190
 149 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 150 195 200 205
 153 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 154 210 215 220
 157 Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 158 225 230 235
 161 <210> SEQ ID NO: 3
 162 <211> LENGTH: 447
 163 <212> TYPE: DNA
 164 <213> ORGANISM: Rattus norvegicus
 166 <220> FEATURE:
 167 <221> NAME/KEY: CDS
 168 <222> LOCATION: (1)..(444)
 169 <223> OTHER INFORMATION:
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 174 Ala Asp Gln Leu Thr Glu Glu Gln Ile Ala Glu Phe Lys Glu Ala Phe
 175 1 5 10 15
 177 tcc cta ttt gac aag gac ggg gat ggg aca ata aca acc aag gag ctg 96
 178 Ser Leu Phe Asp Lys Asp Gly Asp Gly Thr Ile Thr Thr Lys Glu Leu
 179 20 25 30
 181 ggg acg gtg atg cgg tct ctg ggg cag aac ccc aca gaa gca gag ctg 144
 182 Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu Leu
 183 35 40 45
 185 cag gac atg atc aat gaa gta gat gcc gac ggt aat ggc aca atc gac 192
 186 Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile Asp
 187 50 55 60
 189 ttc cct gaa ttc ctg aca atg atg gca aga aaa atg aaa gac aca gac 240
 190 Phe Pro Glu Phe Leu Thr Met Met Ala Arg Lys Met Lys Asp Thr Asp
 191 65 70 75 80
 193 agt gaa gaa gaa att aga gaa gcg ttc cgt gtg ttt gat aag gat ggc 288
 194 Ser Glu Glu Glu Ile Arg Glu Ala Phe Arg Val Phe Asp Lys Asp Gly
 195 85 90 95
 197 aat ggc tac atc agt gca gca gag ctt cgc cac gtg atg aca aac ctt 336
 198 Asn Gly Tyr Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn Leu
 199 100 105 110
 201 gga gag aag tta aca gat gaa gag gtt gat gaa atg atc agg gaa gca 384
 202 Gly Glu Lys Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg Glu Ala
 203 115 120 125
 205 gac atc gat ggg gat ggt cag gta aac tac gaa gag ttt gta caa atg 432
 206 Asp Ile Asp Gly Asp Gly Gln Val Asn Tyr Glu Glu Phe Val Gln Met
 207 130 135 140
 209 atg aca gcg aag tga 447
 210 Met Thr Ala Lys
 211 145
 214 <210> SEQ ID NO: 4
 215 <211> LENGTH: 148

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216 <212> TYPE: PRT
217 <213> ORGANISM: Rattus norvegicus
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225 Ser Leu Phe Asp Lys Asp Gly Asp Gly Thr Ile Thr Thr Lys Glu Leu
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229 Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu Leu
230 35 40 45
233 Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile Asp
234 50 55 60
237 Phe Pro Glu Phe Leu Thr Met Met Ala Arg Lys Met Lys Asp Thr Asp
238 65 70 75 80
241 Ser Glu Glu Glu Ile Arg Glu Ala Phe Arg Val Phe Asp Lys Asp Gly
242 85 90 95
245 Asn Gly Tyr Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn Leu
246 100 105 110
249 Gly Glu Lys Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg Glu Ala
250 115 120 125
253 Asp Ile Asp Gly Asp Gly Gln Val Asn Tyr Glu Glu Phe Val Gln Met
254 130 135 140
257 Met Thr Ala Lys
258 145
261 <210> SEQ ID NO: 5
262 <211> LENGTH: 63
263 <212> TYPE: DNA
264 <213> ORGANISM: Artificial Sequence
266 <220> FEATURE:
267 <223> OTHER INFORMATION: Synthetic DNA
269 <220> FEATURE:
270 <221> NAME/KEY: CDS
271 <222> LOCATION: (1)..(63)
272 <223> OTHER INFORMATION:
275 <400> SEQUENCE: 5
276 tca tca cgt cgt aag tgg aat aag aca ggt cac gca gtc aga gct ata 48
277 Ser Ser Arg Arg Lys Trp Asn Lys Thr Gly His Ala Val Arg Ala Ile
278 1 5 10 15
280 ggt cgg ctg agc tca
281 Gly Arg Leu Ser Ser
282 20
285 <210> SEQ ID NO: 6
286 <211> LENGTH: 21
287 <212> TYPE: PRT
288 <213> ORGANISM: Artificial Sequence
290 <220> FEATURE:
291 <223> OTHER INFORMATION: Synthetic DNA
293 <400> SEQUENCE: 6
295 Ser Ser Arg Arg Lys Trp Asn Lys Thr Gly His Ala Val Arg Ala Ile
296 1 5 10 15

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299 Gly Arg Leu Ser Ser
300 20
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304 <211> LENGTH: 1251
305 <212> TYPE: DNA
306 <213> ORGANISM: Artificial Sequence
308 <220> FEATURE:
309 <223> OTHER INFORMATION: Synthetic DNA
311 <220> FEATURE:
312 <221> NAME/KEY: CDS
313 <222> LOCATION: (1)..(1248)
314 <223> OTHER INFORMATION:
317 <400> SEQUENCE: 7
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319 Met Val Asp Ser Ser Arg Arg Lys Trp Asn Lys Thr Gly His Ala Val
320 1 5 10 15
322 aga gct ata ggt cgg ctg agc tca ctc gag aac gtc tat atc atg gcc 96
323 Arg Ala Ile Gly Arg Leu Ser Ser Leu Glu Asn Val Tyr Ile Met Ala
324 20 25 30
326 gac aag cag aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac 144
327 Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn
328 35 40 45
330 atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag aac acc 192
331 Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr
332 50 55 60
334 ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc 240
335 Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser
336 65 70 75 80
338 acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg 288
339 Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met
340 85 90 95
342 gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac 336
343 Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp
344 100 105 110
346 gag ctg tac aag ggc ggt acc gga ggg agc atg gtg agc aag ggc gag 384
347 Glu Leu Tyr Lys Gly Gly Thr Gly Ser Met Val Ser Lys Gly Glu
348 115 120 125
350 gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc gag ctg gac ggc gac 432
351 Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp
352 130 135 140
354 gta aac ggc cac aag ttc agc gtg tcc ggc gag ggc gac gat gcc 480
355 Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala
356 145 150 155 160
358 acc tac ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg 528
359 Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu
360 165 170 175
362 ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg acc tac ggc gtg cag 576
363 Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln
364 180 185 190

VERIFICATION SUMMARY

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